NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

| 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990. |
|---|
| 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c). |
| 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e). |
| 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing." |
| 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d). |
| 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e). |

Other: Seg 1D 5 is Reversed Polarity

Applicant must provide:

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

RAW SEQUENCE LISTING PATENT APPLICATION US/08/423,194

DATE: 11/29/95 TIME: 15:11:35

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This Raw Listing contains the General Information Section and up to the first 5 pages.

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SEQUENCE LISTING
 1
 2
 3
            General Information:
     (1)
                                                         ENTERED
 5
        (i) APPLICANT: Eaton, Dan L.
                        de Sauvage, Frederic J.
 7
 8
       (ii) TITLE OF INVENTION: MPL LIGAND
 9
10
      (iii) NUMBER OF SEQUENCES: 77
11
12
       (iv) CORRESPONDENCE ADDRESS:
13
             (A) ADDRESSEE: Genentech, Inc.
             (B) STREET: 460 Point San Bruno Blvd
14
15
             (C) CITY: South San Francisco
             (D) STATE: California
16
17
             (E) COUNTRY: USA
18
             (F) ZIP: 94080
19
20
        (V) COMPUTER READABLE FORM:
21
             (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
             (B) COMPUTER: IBM PC compatible
22
23
             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24
             (D) SOFTWARE: patin (Genentech)
25
26
       (vi) CURRENT APPLICATION DATA:
27
             (A) APPLICATION NUMBER: 08/423194
28
             (B) FILING DATE: 18-APR-1995
29
             (C) CLASSIFICATION:
30
. 31
      (vii) PRIOR APPLICATION DATA:
32
             (A) APPLICATION NUMBER: 08/249376
33
             (B) FILING DATE: 25-MAY-1994
34
35
      (vii) PRIOR APPLICATION DATA:
             (A) APPLICATION NUMBER: 08/223263
36
37
             (B) FILING DATE: 04-APR-1994
38
39
      (vii) PRIOR APPLICATION DATA:
             (A) APPLICATION NUMBER: 08/196689
40
41
             (B) FILING DATE: 15-FEB-1994
42
43
      (vii) PRIOR APPLICATION DATA:
44
             (A) APPLICATION NUMBER: 08/185607
45
             (B) FILING DATE: 21-JAN-1994
46
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/423,194

DATE: 11/29/95 TIME: 15:11:39

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47
     (vii) PRIOR APPLICATION DATA:
48
            (A) APPLICATION NUMBER: 08/176553
49
            (B) FILING DATE: 03-JAN-1994
50
     (viii) ATTORNEY/AGENT INFORMATION:
51
52
            (A) NAME: Winter, Daryl B.
            (B) REGISTRATION NUMBER: 32,637
53
            (C) REFERENCE/DOCKET NUMBER: 871P4D2
54
55
       (ix) TELECOMMUNICATION INFORMATION:
56
            (A) TELEPHONE: 415/225-1249
57
58
            (B) TELEFAX: 415/952-9881
59
            (C) TELEX: 910/371-7168
60
    (2) INFORMATION FOR SEQ ID NO:1:
61
62
63
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 353 amino acids
64
65
            (B) TYPE: amino acid
66
           (D) TOPOLOGY: linear
67
68
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70
     Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
71
     -21 -20
                              -15
72
73
     Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
74
75
76
     Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
77
                           15
78
79
     Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
80
                           30
81
82
     Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
83
84
85
     Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
86
87
88
     Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
89
                           75
90
91
     Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
92
93
94
     Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
95
                          105
96
97
     Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
98
                          120
99
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/423,194

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|------------|---|--|---------------------|--|---|-----------------------------|---|---|--|--|----------|--|---|--------|
| Ser 130 | Phe | Gln | His | Leu | Leu 135 | Arg | Gly | Lys | Val | Arg 140 | Phe | Leu | Met | Leu |
| | ~ 7 | a 1 | ~ | m 1 | • | | ••- • | • | . | | n | D | m1 | m\ |
| | стА | стА | ser | ınr | | cys | vaı | Arg | Arg | | PIO | Pro | unr | Thr |
| 145 | | | | | 120 | | | | | 123 | | | | |
| 810 | Wal. | Dwo | Cor | X ~~~ | mb ~ | C0.T | T 011 | Val | T 011 | mh ~ | T 011 | 1 ~ ~ | <i>α</i> 1 | T 011 |
| | vaı | PIO | ser | AIG | | Ser | Leu | vaı | neu | | Leu | ASII | GIU | Leu |
| 100 | | | | • | 163 | | | | | 1/0 | | | | |
| Dro | Nen | λrα | Thr | Sor | G1 v | T 611 | T (2) 1 | Gl 11 | Thr | λen | Dha | Thr | λla | Sor |
| | ASII | Alg | 1111 | 261 | - | пец | nea | GIU | 1111 | | rne | 1111 | ATG | Ser |
| 1,5 | | | | | 100 | | | | | 103 | | | | |
| Δla | Δra | Thr | Thr | Glv | Ser | Glv | T.e.i | T.e.11 | I.vs | Trn | Gln | Gln | Glv | Phe |
| | 9 | | | 1 | | , | | | -1- | _ | | | - | |
| | | | | | | | | | | | | | | |
| Ara | Ala | Lvs | Ile | Pro | Glv | Leu | Leu | Asn | Gln | Thr | Ser | Ara | Ser | Leu |
| | | -,,- | | | | | | | | 215 | | 3 | | |
| | | | | | | | | | | | | | | |
| Asp | Gln | Ile | Pro | Glv | Tvr | Leu | Asn | Arq | Ile | His | Glu | Leu | Leu | Asn |
| 220 | | | | - | 225 | | | | | 230 | | | | |
| | | | | | | | | | | | | | | |
| Gly | Thr | Arg | Gly | Leu | Phe | Pro | Gly | Pro | Ser | Arg | Arg | Thr | Leu | Gly |
| 235 | | _ | _ | | 240 | | _ | | | 245 | _ | | | _ |
| | | | | | | | • | | | | | | | |
| Ala | Pro | Asp | Ile | Ser | Ser | Gly | Thr | Ser | Asp | Thr | Gly | Ser | Leu | Pro |
| 250 | | | | | 255 | | | | | 260 | | | | |
| | • | | | | | | | | | | | | | |
| Pro | Asn | Leu | Gln | Pro | Gly | Tyr | Ser | Pro | Ser | Pro | Thr | His | Pro | Pro |
| 265 | | | | | 270 | | | | | 275 | | | | |
| | | | | | | | | | | | | | | |
| | Gly | Gln | Tyr | Thr | | Phe | Pro | Leu | Pro | | Thr | Leu | Pro | Thr |
| 280 | | | | | 285 | | | | | 290 | | | | |
| _ | | | | _ | ' | _ | _ | _ | _ | _ | | _ | | _ |
| | Val | Val | GIn | Leu | | Pro | Leu | Leu | Pro | | Pro | Ser | АТа | Pro |
| 295 | | | | | 300 | | | | | 305 | | | | |
| mb | D | m\ | D | m\ | a | D | T | . | 3 | m1 | ~ | | m\ | 77.i ~ |
| | Pro | Thr | Pro | Thr | | PIO | Leu | Leu | ASN | | ser | туг | Thr | HIS |
| 210 | | | | | 313 | | | | | 320 | | | | |
| Sor | al n | λan | Lan | Sor | Gl n | alu | G] v | | | | | | | |
| | GIII | ASII | ьец | 261 | | GIU | - | | | | | | | |
| 323 | | | | | 330 | | J J Z | | | | | | | |
| (2) | INFO | יים אי | TON 1 | OR S | SEO 1 | או מז | 1:2: | | | | | | | |
| (-, - | | | | . 01. | JUQ . | | | | | | | | | |
| ι. | i) SI | COUE | NCE (| CHARA | ACTE | RIST | rcs: | | | | | | | |
| `` | - | | | | | | | | | | | | | |
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| (x: | i) SI | EQUE | NCE I | DESC | RIPT | ON: | SEQ | ID 1 | 10:2 | : | | | | |
| • | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | 130 Val 145 Ala 160 Pro 175 Ala 190 Arg 205 Asp 220 Gly 235 Ala 250 Pro 265 Thr 280 Pro 295 Thr 310 Ser 325 (2) | 130 Val Gly 145 Ala Val 160 Pro Asn 175 Ala Arg 190 Arg Ala 205 Asp Gln 220 Gly Thr 235 Ala Pro 250 Pro Asn 265 Thr Gly 280 Pro Val 295 Thr Pro 310 Ser Gln 325 (2) INFORM (1) (1) (1) (2) (1) (2) (3) | Nal Gly Gly 145 | Val Gly Gly Ser 145 Ala Val Pro Ser 160 Pro Asn Arg Thr 175 Ala Arg Thr Thr 190 Arg Ala Lys Ile 205 Asp Gln Ile Pro 220 Gly Thr Arg Gly 235 Ala Pro Asp Ile 250 Pro Asn Leu Gln 265 Thr Gly Gln Tyr 280 Pro Val Val Gln 295 Thr Pro Thr Pro 310 Ser Gln Asn Leu 325 (2) INFORMATION I | Val Gly Gly Ser Thr 145 Ala Val Pro Ser Arg 160 Pro Asn Arg Thr Ser 175 Ala Arg Thr Thr Gly 190 Arg Ala Lys Ile Pro 205 Asp Gln Ile Pro Gly 220 Gly Thr Arg Gly Leu 235 Ala Pro Asp Ile Ser 250 Pro Asn Leu Gln Pro 265 Thr Gly Gln Tyr Thr 280 Pro Val Val Gln Leu 295 Thr Pro Thr Pro Thr 310 Ser Gln Asn Leu Ser 325 (2) INFORMATION FOR Ser (A) LENGTH: 17 (B) TYPE: nucl (C) STRANDEDNE (D) TOPOLOGY: | Val Gly Gly Ser Thr Leu 145 | Val Gly Gly Ser Thr Leu Cys 145 Val Gly Gly Ser Thr Leu Cys 145 Ala Val Pro Ser Arg Thr Ser 160 Pro Asn Arg Thr Ser Gly Leu 175 Ala Arg Thr Thr Gly Ser Gly 190 Arg Ala Lys Ile Pro Gly Leu 205 Gly Thr Arg Gly Leu Phe Pro 235 Pro Asn Leu Gln Pro Gly Tyr 265 Pro Val Val Gln Leu His Pro 295 Thr Pro Thr Pro Thr Ser Pro 310 Ser Gln Asn Leu Ser Gln Glu 325 (1) SEQUENCE CHARACTERIST: (A) LENGTH: 1795 bases (B) Type: nucleic acid (C) STRANDEDNESS: sing (D) TOPOLOGY: linear | Val Gly Gly Ser Thr Leu Cys Val 145 Ala Val Pro Ser Arg Thr Ser Leu 160 Pro Asn Arg Thr Ser Gly Leu Leu 175 Ala Arg Thr Thr Gly Ser Gly Leu 190 Arg Ala Lys Ile Pro Gly Leu Leu 210 Asp Gln Ile Pro Gly Tyr Leu Asn 225 Gly Thr Arg Gly Leu Phe Pro Gly 240 Ala Pro Asp Ile Ser Ser Gly Thr 250 Pro Asn Leu Gln Pro Gly Tyr Ser 270 Thr Gly Gln Tyr Thr Leu Phe Pro 280 Pro Val Val Gln Leu His Pro Leu 300 Thr Pro Thr Pro Thr Ser Pro Leu 310 Ser Gln Asn Leu Ser Gln Glu Gly 325 Ser Gln Asn Leu Ser Gln Glu Gly 325 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1795 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | Val Gly Gly Ser Thr Leu Cys Val Arg 145 Nal Gly Gly Ser Thr Leu Cys Val Arg 150 Ala Val Pro Ser Arg Thr Ser Leu Val 160 Pro Asn Arg Thr Ser Gly Leu Leu Glu 175 Ala Arg Thr Thr Gly Ser Gly Leu Leu 190 Arg Ala Lys Ile Pro Gly Leu Leu Asn 205 Asp Gln Ile Pro Gly Tyr Leu Asn Arg 220 Gly Thr Arg Gly Leu Phe Pro Gly Pro 235 Pro Asn Leu Gln Pro Gly Tyr Ser Pro 250 Thr Gly Gln Tyr Thr Leu Phe Pro Leu 280 Pro Val Val Gln Leu His Pro Leu 285 Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu 310 Ser Gln Asn Leu Ser Gln Glu Gly 325 (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1795 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | Val Gly Gly Ser Thr Leu Cys Val Arg Arg 145 Nal Gly Gly Ser Thr Leu Cys Val Arg Arg 150 Ala Val Pro Ser Arg Thr Ser Leu Val Leu 160 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr 175 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys 190 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln 205 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile 220 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser 240 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp 255 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser 265 Pro Val Val Gln Leu His Pro Leu Pro 280 Thr Pro Thr Pro Thr Ser Pro Leu Pro 300 Thr Pro Thr Pro Thr Ser Gln Glu Gly 325 Ser Gln Asn Leu Ser Gln Glu Gly 330 Ser Gln Asn Leu Ser Gln Glu Gly 325 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1795 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | 130 | Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro 145 Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu 160 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe 175 Ala Arg Thr Thr Gly Ser Gly Leu Leu Leu Lys Trp Gln 190 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser 210 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu 225 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu 225 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg 245 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly 255 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr 280 Pro Val Val Gln Leu His Pro Leu Pro Pro Thr 290 Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser 310 Ser Gln Asn Leu Ser Gln Glu Gly 332 (2) INFORMATION FOR SEQ ID NO:2: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1795 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro 145 Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn 160 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr 175 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln 190 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg 205 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu 220 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr 235 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser 255 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His 265 Pro Val Val Gln Leu His Pro Leu Pro Pro Thr Leu 280 Thr Pro Thr Pro Thr Ser Gln Glu Gly 330 Ser Gln Asn Leu Ser Gln Glu Gly 332 (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1795 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | Ser |

RAW SEQUENCE LISTING PATENT APPLICATION US/08/423,194

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| | | | | | A 1. | 11 U 1 U 1 |
|------------|---------------------|-------------|--------------|-------------------|-------------------|------------|
| 153 154 | TCTTCCTACC | CATCTGCTCC | CCAGAGGGCT | GCCTGCTGTG | CACTTGGGTC | 50 |
| 155 | | | | | | |
| 156 | CTGGAGCCCT | TCTCCACCCG | GATAGATTCC | TCACCCTTGG | CCCGCCTTTG | 100 |
| 157 | | | | | | |
| | | | | | | |
| 158 | | | | | | |
| 159 | CCCCACCCTA | CTCTGCCCAG | AAGTGCAAGA | GCCTAAGCCG | CCTCCATGGC | 150 |
| 160 | | | | | | |
| 161 | | | | | | |
| 162 | CCCAGGAAGG | ATTCAGGGGA | GAGGCCCCAA | ACAGGGAGCC | ACGCCAGCCA | 200 |
| 163 | | | | | | |
| 164 | | | | | | |
| | a. a. aaaaaa | GG1G11EGG1 | COMO LOMO LA | mmaamaamaa | ПОСТОВНОСТ | 250 |
| 165 | GACACCCCGG | CCAGAATGGA | GCTGACTGAA | TIGCTCCTCG | TGGTCATGCT | 250 |
| 166 | | | | | • | |
| 167 | | | | | | |
| 168 | TCTCCTAACT | GCAAGGCTAA | CGCTGTCCAG | CCCGGCTCCT | CCTGCTTGTG | 300 |
| 169 | | | | | | |
| 170 | | | | | | |
| 171 | A COMOCO A CM | CCTCACTAAA | OTTO OTTO | A CITICO CA TICOT | CCTTCACAGC | 250 |
| | ACCICCGAGI | CCICAGIAAA | CIGCIICGIG | ACTCCCATGT | CCTTCACAGC | 330 |
| 172 | | | | | | |
| 173 | | | | | | |
| 174 | AGACTGAGCC | AGTGCCCAGA | GGTTCACCCT | TTGCCTACAC | CTGTCCTGCT | 400 |
| 175 | | | | | | |
| 176 | | | | | | |
| 177 | GCCTGCTGTG | GACTTTAGCT | TGGGAGAATG | GAAAACCCAG | ATGGAGGAGA | 450 |
| 178 | 0001001010 | | 1000 | •••••• | | |
| | | | | | | |
| 179 | | | | | | |
| 180 | CCAAGGCACA | GGACATTCTG | GGAGCAGTGA | CCCTTCTGCT | GGAGGGAGTG | 500 |
| 181 | | | | | | |
| 182 | | | | | | |
| 183 | ATGGCAGCAC | GGGGACAACT | GGGACCCACT | TGCCTCTCAT | CCCTCCTGGG | 550 |
| 184 | | | | | | |
| 185 | | | | | | |
| 186 | СС <u>АССТТТТСТ</u> | GGACAGGTCC | מחכחככתכת | таааасссста | CAGAGCCTCC | 600 |
| 187 | OCAGCIIICI | OUNCAGGICC | 0101001001 | 1000000010 | CHOROCCICC | |
| | | | | | | |
| 188 | | | | | | |
| 189 | TTGGAACCCA | GCTTCCTCCA | CAGGGCAGGA | CCACAGCTCA | CAAGGATCCC | 650 |
| 190 | | | | | | |
| 191 | | | | | | |
| 192 | AATGCCATCT | TCCTGAGCTT | CCAACACCTG | CTCCGAGGAA | AGGTGCGTTT | 700 |
| 193 | | | | | | |
| 194 | | | | | | |
| 195 | ССТСАТССТТ | стассассст | ССУСССТСТС | CCTCACCCCC | GCCCCACCCA | 750 |
| 196 | CCIGAIGCII | GIAGGAGGGI | CCACCCICIG | CGICAGGCGG | GCCCCACCCA | 750 |
| | | | | | | |
| 197 | | | | | | |
| 198 | CCACAGCTGT | CCCCAGCAGA | ACCTCTCTAG | TCCTCACACT | GAACGAGCTC | 800 |
| 199 | | | | | | |
| 200 | | | | | | |
| 201 | CCAAACAGGA | CTTCTGGATT | GTTGGAGACA | AACTTCACTG | CCTCAGCCAG | 850 |
| 202 | | | | | | |
| 203 | | | | | | |
| | A A CITTA CITTA CA | mamaaaaamma | max x amaaas | 0010001mm | 2020001101 | 000 |
| 204 | AACTACTGGC | TCTGGGCTTC | TGAAGTGGCA | GCAGGGATTC | AGAGCCAAGA | 900 |
| 205 | | | | | | |
| | | | | | | |

RAW SEQUENCE LISTING PATENT APPLICATION US/08/423,194

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|-------------------|-------------|------------|-------------|------------|-------------------|--------|
| 206 207 208 | TTCCTGGTCT | GCTGAACCAA | ACCTCCAGGT | CCCTGGACCA | AATCCCCGGA | 950 |
| 209 210 | TACCTGAACA | GGATACACGA | ACTCTTGAAT | GGAACTCGTG | GACTCTTTCC | 1000 |
| 211 212 | шаал ааашал | aaabaabaaa | ma coa coco | | maraan ran m | 1050 |
| 213 214 215 | TGGACCCTCA | CGCAGGACCC | TAGGAGCCCC | GGACATTTCC | TCAGGAACAT | 1050 |
| 216 217 | CAGACACAGG | CTCCCTGCCA | CCCAACCTCC | AGCCTGGATA | TTCTCCTTCC | 1100 |
| 218 219 220 | CCAACCCATC | CTCCTACTGG | ACAGTATACG | СТСТТСССТС | TTCCACCCAC | 1150 |
| 221 222 223 | CTTGCCCACC | CCTGTGGTCC | AGCTCCACCC | CCTGCTTCCT | GACCCTTCTG | 1200 |
| 224 225 226 | CTCCAACGCC | CACCCCTACC | AGCCCTCTTC | TAAACACATC | CTACACCCAC | 1250 |
| 227 228 229 | TCCCAGAATC | TGTCTCAGGA | AGGGTAAGGT | TCTCAGACAC | TGCCGACATC | 1300 |
| 230 231 232 | AGCATTGTCT | CATGTACAGC | TCCCTTCCCT | GCAGGGCGCC | CCTGGGAGAC | 1350 |
| 233 234 235 | AACTGGACAA | GATTTCCTAC | TTTCTCCTGA | AACCCAAAGC | CCTGGTAAAA | 1400 |
| 236 237 238 | GGGATACACA | GGACTGAAAA | GGGAATCATT | TTTCACTGTA | CATTATAAAC | 1450 |
| 239 240 241 | CTTCAGAAGC | ТАТТТТТТТА | AGCTATCAGC | AATACTCATC | AGAGCAGCTA | 1500 |
| 242 243 244 | GCTCTTTGGT | CTATTTCTG | CAGAAATTTG | CAACTCACTG | ATTCTCTACA | 1550 |
| 245 246 247 | TGCTCTTTTT | CTGTGATAAC | TCTGCAAAGG | CCTGGGCTGG | CCTGGCAGTT | 1600 |
| 248 249 250 | GAACAGAGGG | AGAGACTAAC | CTTGAGTCAG | AAAACAGAGA | AAGGGTAATT | 1650 |
| 251 252 253 | TCCTTTGCTT | CAAATTCAAG | GCCTTCCAAC | GCCCCCATCC | CCTTTACTAT | 1700 |
| 254 255 256 | CATTCTCAGT | GGGACTCTGA | TCCCATATTC | TTAACAGATC | TTTACTCTTG | 1750 |
| 257 258 | AGAAATGAAT | AAGCTTTCTC | TCAGAAAAA | AAAAAAAAA | AAAAA 1795 | |

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/423,194

DATE: 11/29/95 TIME: 15:11:52

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Original Text

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Wrong application Serial Number

(A) APPLICATION NUMBER: 08/423194